



New Magic-BLAST (v1.5.0) is now available!

Magic-BLAST, the BLAST tool that aligns next generation sequencing reads, has just been released with new user driven enhancements.

Release 1.5.0 adds these features:

- Nanopore sequence alignment
- Improved multithreading performance
- Support for the new BLAST database version, [BLASTDBv5](#), that allows you to limit your search by taxonomy
- More reliable placements of reads

A new [paper](#) (PMID: [31345161](#)), published in July 2019 by BMC Bioinformatics, describes Magic-BLAST and compares it to other popular aligners.

Get Magic-BLAST at <https://ncbi.github.io/magicblast/>

BLAST+2.10.0 is here!

Improved support for computation-based statistics

Composition-based statistics applies to protein-protein comparisons (including translated DNA like BLASTX) and takes the composition of the subject sequence into account during the final step of BLAST. We have updated the BLAST process to improve the stability of BLAST results against changes in the number of results requested.

In addition, the new version generates databases in version 5 format by default and fixes several bugs. See the release notes for more details:

<https://www.ncbi.nlm.nih.gov/books/NBK131777/>

The new executables are at :

<https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST>

Also, there is a new Docker image:

<https://hub.docker.com/r/ncbi/blast>

Let us know what you think.

blast-help@ncbi.nlm.nih.gov

Primer-BLAST Enhanced

Improved primer selection

Sometimes Primer-BLAST can't design specific primers for your target sequence because of similar non-target sequences in the database. In some cases, you may know that these non-target matches are not important to your research and are safe to ignore. You can now choose to allow certain off-target matches. This gives Primer-BLAST greater freedom in primer selection and a better chance of finding highly specific primers.

You can re-search for specific primers by accepting some of the unintended targets, check the box(es) next to the ones you accept and try again to re-search for specific primers. ☐ Submit

Primer pair 1		Sequence (5'→3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer		AGAAGGTGAAGATGCGGTG	Plus	20	10	29	60.04	55.00	2.00	0.00
Reverse primer		GTCCTTGGTCATGTGGGAGG	Minus	20	125	106	60.04	60.00	4.00	2.00
Product length 116										
Products on intended targets										
>NM_005004.4 Homo sapiens NADH:ubiquinone oxidoreductase subunit B8 (NDUFB8), transcript variant 1, mRNA										
product length = 116										
Forward primer	1	AGAAGGTGAAGATGCGGTG	20							
Template	10	29							
Reverse primer	1	GTCCTTGGTCATGTGGGAGG	20							
Template	125	106							
Products on potentially unintended templates										
>NM_001284367.1 Homo sapiens NADH:ubiquinone oxidoreductase subunit B8 (NDUFB8), transcript variant 2, mRNA										
product length = 116										
Forward primer	1	AGAAGGTGAAGATGCGGTG	20							
Template	62	81							
Reverse primer	1	GTCCTTGGTCATGTGGGAGG	20							

New videos
on YouTube

- Improved Standalone BLAST database and programs: now with taxonomic information
- Getting the Most out of Web BLAST Tabular Format
- Getting the Genomic Context for BLAST Protein Matches
- Five Teaching Examples on how to use NCBI BLAST



<https://bit.ly/2MFzsR6>



U.S. National Library of Medicine
National Center for Biotechnology Information